CLAIMS:

sub A7

1. A DNA sequence which is (a) at least part of the sequence set out in the appended sequence listing; or (b) a variant of a sequence (a) which encodes a polypeptide which is at least 80%, preferably at least 90%, identical with the corresponding peptide as set out in table II; provided that it is not a sequence encoding all or part of the polypeptide consisting of amino acids 1-920 encoded by *mon AI* as set out in table II.

2. A DNA sequence according to claim 1 comprising the complete monensin gene cluster or a variant thereof.

3. A DNA sequence encoding at least part of at least one polypeptide which is necessary for the biosynthesis of monensin, and which is encoded by DNA included in the appended sequence listing or an allele, mutation or other variant thereof; provided that said polypeptide is not all or part of amino acids 1-920 encoded by *mon AI* as set out in table II.

4. A DNA sequence according to claim 3 which comprises at least part of one or more of the following genes: *mon BI, mon BII, mon CI, mon CII, mon H, mon RI, mon RII, mon T, mon AIX* and *mon AX*.

5. A DNA sequence according to claim 4 comprising all of the genes listed therein or an allele, mutation or other variant thereof.

6. A DNA sequence according to claim 3 encoding at least part of one or more of the polypeptides set out below, said polypeptide having the amino acid sequence as set out in the appended sequence data or being a variant thereof having the specified activity:

peptide	activity
mon CII	epoxyhydrolase/cyclase
mon E	S-adenosylmethionine-dependent methyltransferase
mon T	monensin resistance gene
mon RII	repressor protein
mon AIX	thioesterase
mon AI	polyketide synthase multienzyme
mon AII	polyketide synthase multienzyme
mon AIII	polyketide synthase multienzyme
mon AIV	polyketide synthase multienzyme
mon AV	polyketide synthase multienzyme
mon AVI	polyketide synthase multienzyme
mon AVII	polyketide synthase multienzyme
mon AVIII	polyketide synthase multienzyme
mon H	regulatory protein
mon CI	flavin-dependent epoxidase
mon BII	carbon-carbon double bond isomerase

mon BI carbon-carbon double bond isomerase

mon D cytochrome P450 hydroxylase

mon RI activator protein

mon AX thioesterase

7. A DNA sequence according to claim 6 encoding a single enzyme activity of a multienzyme encoded by any of *mon AI-mon AVIII* or a variant or part thereof.

8. A DNA sequence according to any preceding claim encoding any one or more of the domains as set out in Table I or a variant or part thereof.

9. A DNA sequence according to any preceding claim which has a length of at least 30, preferably at least 60, bases.

10. A recombinant cloning or expression vector comprising a DNA sequence according to any preceding claim.

11. A transformant host cell which has been transformed to contain a DNA sequence according to any of claims 1-9 and which is capable of expressing a corresponding polypeptide.

12. A hybridisation probe which is a DNA sequence according to any of claims 1-9.

13. Use of a probe according to claim 12 to detect a PKS cluster, optionally followed by isolation of the detected cluster.

14. Use of a probe according to claim 12 which encodes at least part of a polypeptide having a known function to detect genes encoding polypeptides having analogous function.

15. Use according to claim 14 wherein the polypeptide of known function is AT of module 5 or the regulatory protein encoded by *mon RI*.

16. A hybridization probe comprising a polynucleotide which binds specifically to a region of the monensin gene cluster selected from *mon BI, mon BII, mon CI, mon CII, mon H, mon RI, mon RII, mon T, mon AIX* and *mon AX*.

17. Use of a probe according to claim 16 in a method of detecting the presence of a gene cluster which governs the synthesis of a polyether, and optionally isolating a gene cluster detected thereby.

18. Use of a probe according to claim 12 which comprise a polynucleotide which binds specifically to a gene responsible for levels of activity of the monensin gene cluster, in a method of detecting an analogous gene in a gene cluster for biosynthesis of another polyketide, optionally followed by a step of manipulating the gene detected thereby to alter the level of expression of said other polyketide.

19. Use according to claim 18 wherein the gene is a regulatory gene, resistance gene or thioesterase gene.

20. Use of the *mon RI* gene or variant and a monensin promoter to control expression of a heterologous gene in *S. cinnamonensis*.

21. Use of a portion of the monensin gene cluster encoding a polypeptide having chain terminating activity, preferably comprising at least one of *mon AIX* and *mon AX* or a mutant, allele or other variant thereof encoding a polypeptide having chain terminating activity, to effect chain release of a peptide other than monensin.

22. Use of a portion of the monensin gene cluster encoding a polypeptide having carbon-carbon double bond isomerase activity, preferably comprising at least one of

mon BI and *mon BII* or a mutant, allele or other variant thereof having isomerase activity to provide a desired stereochemical outcome in the synthesis of a polyketide other than monensin.

23. A polypeptide encoded by a portion of the monensin gene cluster, preferably comprising at least one of *mon BI* and *mon BII* or a mutant, allele or other variant thereof, having carbon-carbon double bond isomerase activity, or at least one of *mon AIX* and *mon AX* or a mutant, allele or other variant thereof having chain terminating activity.

24. An epoxidase enzyme encoded by *mon CI* or a derivative or variant thereof having epoxidase activity.

25. A cyclase enzyme encoded by *mon CII* or a derivative or variant thereof having cyclase activity.

26. Use of a portion of the monensin gene cluster encoding a peptide having epoxidase or cyclase activity, preferably comprising *mon CI* or *mon CII* or a mutant, allele or other variant thereof encoding a polypeptide having epoxidase or cyclase activity to provide a said activity in the biosynthesis of a polypeptide other than monensin.

27. A process for producing a polyketide containing a desired starter unit comprising providing a PKS gene having a loading module and a plurality of extension modules, wherein the loading module includes a KS_q domain derived from a KS domain of a monensin extension module.

28. A process according to claim 27 wherein the KS_q domain is derived from KS of module 5 of monensin.

SUB A5

29. A process according to claim 27 or claim 28 wherein the starter unit also includes an AT_q domain derived from an AT domain which is naturally associated with the KS domain.

30. A DNA sequence comprising DNA encoding at least one PKS loading module and a plurality of PKS extension modules, and which can be expressed to produce a polyketide; wherein at least one of said modules or at least one domain thereof is a monensin module or domain or a variant thereof and is contiguous to a further one of said modules or a domain to which it is not naturally contiguous; provided that the sequence is not an *ery* loading module, the first and second extension modules of the *ery* PKS and the *ery* chain-terminating thioesterase in which the DNA encoding AT of the first extension module has been substituted by DNA encoding an ethyl malonyl-CoA

AT from the monensin gene cluster.

31. A DNA sequence according to claim 30 wherein said further module or domain is also a monensin module or domain or variant thereof.

32. A DNA sequence according to claim 30 wherein said further module or domain is a module or domain of a PKS of a polyketide other than monensin or a variant thereof.

Sub A6 33. A DNA sequence according to claim 30, 31 or 32 wherein said loading module is adapted to load a starter unit other than a starter unit normally received by the adjacent extension module.

34. A DNA sequence according to claim 33 wherein said loading module is derived from a monensin extension module or variant thereof.

Sub A7 35. A polyketide synthase encoded by the DNA sequence of any of claims 30-34.

36. A polyketide compound as produced by a synthase according to claim 35.

37. A vector containing a DNA sequence of any of claims 30-34.

38. A transformant cell transformed to contain a DNA sequence of any of claims 30-34.

39. A method of producing *S. cinnamonensis* capable of enhanced levels of production of monensin comprising engineering it to overexpress the *mon RI* gene.

40. A method according to claim 39 wherein said engineering comprises introducing at least one additional copy of the *mon RI* gene as shown in the appended sequence data or a variant thereof.

41. *S. cinnamonensis* containing multiple copies of the *mon RI* gene as shown in the appended sequence data and/or variant(s) thereof.

42. A method of producing monensin comprising culturing the organism of claim 41 and/or an organism produced by the method of claim 39 or claim 40.

43. A process for expressing a gene heterologous to *S. cinnamonensis* comprising transforming *S. cinnamonensis* with DNA encoding a heterologous gene and expressing said

gene under control of the activator gene *mon RI* or actII/orf4.

44. A process according to claim 43 wherein said heterologous gene is a PKS gene.

45. 13-Propyl erythromycin A.

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